

**Fig. 1**

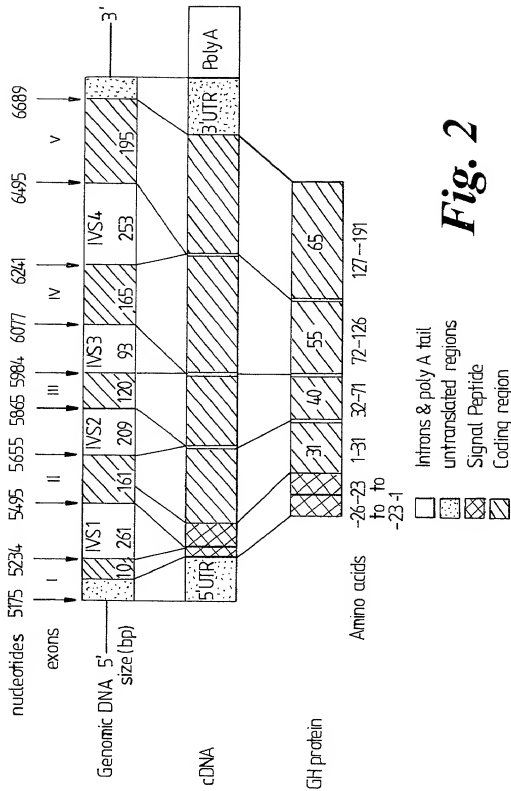


Fig. 2



Figure 4

1-75	cccatgoccatggttgaagggcaagggtctgggtggtcctcttttagatctttggactaggcctcggaacctgataa
5	gggtacggtaccaaacctcgtctctccagaccaccaggagaaactctagaacggatccggagcctggactatt
76-150	gggtggggggccactctcaaggggttcaggccaggacctgagccacgaagtccagggccaggaggttaagggtttcca
151-225	ccaccocgggtgagagtctcccaagtcgggtctcgtgactcgggtcgtctcagtcocggctctcccaatctccaaagt
226-300	tcocaggaacagcccggtccggggagcccccagatgtctctctgttccaaagtcttccaaatgaataaaacatttt
301-375	aggctccttgtcgggcaaggccgctcgggggtctacaagaagaaacaaggctctacaaggtcttactcttttttgtaaa
376-450	ctctgaaaaagctgtcagatgtctcagttcatggaaataaaacagctccagaataataaaactcaactgaggtcagcttg
451-525	gagacttttcgcagactctacaagtcacagtacactttattgtcgagtccttattttgtagttggaactccagtcgaac
526-600	aggcccatggcccgcacatgctggttgagggttggttcgagagagactgaccggggggagtcggggcaaaactctggga
601-675	tcogggtaccocgggctcagcaactcccaaccgactctctctgactgggccccctcaccocggtttttagacccct
676-750	gtctcatctggttttagaaaaactctctctgagccctaaagacagagtcctcttctaactcttggggctagtcctc
751-825	cagagtagccaaatctctttatgagaaggactcggggattgtctgtccaggaaagttaattgaaacccgagtcacagag
826-900	cccaaaagttgggggggtataactgggaagaaggtctgggggcaacagctgttctgtgtgaggttctgtctgtgtatgt
901-975	gggttttcaaccccccatatttgacctttccgaaccccggtgtgcaaaaaacccccccacacacacacacataca
976-1050	gcatgctcacacaggttgtgtgtcctggacctctgggtctggggccctactctggagctggctcttaggggtccagcgg
1051-1125	cgtacagagtgtgtccacacaacaggacctggggaacccaaccccggtgagacctcgacacggatcccgagtcgccc
1126-1200	actgttagggggcagcgaggttgtggggggggcagtttggcacccactcctcaggtgacaggtcgctaaaaactcaga
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1276-1350	aatcacccaataagaactctacaggttaacaaaaaactacctctaccccagaaaaatattgaaataaaaaattt
1351-1425	ttagtgggtgattttctgaataggtccacttggtttttttttgatgacatgggggtcttttaactaactttattttaa

aaaaaa caagt gagaacagctcccactccaggagggaagacacacacatcccgtagacaagatgcagatgt 751-825  
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 5 ggcctttgggcttcattcccatctcgtcgggcagggtatctgtttcaggaggggcggagcagcggggcccca 826-900  
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 cctcccccttctctggagtccttctctctcagctctggggaaggagagaggtcggggtccacaggaccctagac  
 25 ctggggtgctgtgactggggaagacctgctaaagagacgtgggtttgagtcctgacccagcagtgtagcagcc  
 gaccgcagacactgaacctttctggacgattctctgcacccaactcaggactgggtcgtcacatcgtcgg  
 30 aggaacacctccccagggttaccagtggtctctactaagggtggctctgccccaaaggaggagcgtctgcacatg  
 tcccttggagggggtccaaatggtaacaaagagatgattcccacccagacgggggtgctccctcgacagacgtgtac  
 catcagggaatcgcgctggctcaatgacccgtgggtgcctggggcgaggagggtcatttggctgggcaaacagag  
 gtagtcccggttagcgcgaccagagttactggccacccacgagaccgcctcccgtaaacccagccgtttcgctctc

1501-1575

1576-1650

1651-1725

1726-1800

1801-1875

1876-1950

1951-2025

2026-2030

cgagg  
gctcc

PCR primers are marked in **bold** (42-1984 = 1542bp) .  
Sequencing primers are underlined (GHLCR3.1, 541-558; GHLCR3.2, 1006-1023; GHLCR3.3, 2031-2058; GHLCR5.0, 640-658)

Figure 5

	-700	ctgtttcttctg	gtttgtgtct	ctgctgcaag	tccaaggagc	tggggcaata	-651
5	-650	ccttgagtct	gggttctctg	tccccaggga	cctgggggag	ccccagcaat	-601
	-600	gctcaggsga	agggggagag	aaagtgtggg	gttggtttctc	tctagtgtgc	-551
	-550	agtgctggaa	ctgcatccag	ctgaactcag	ctgaccaggag	agtcctcagc	-501
	-500	agaagtggaa	ttccaggactg	aatcgtgtctc	acaaccccca	caatctattg	-451
	-450	ctgtgtcttg	gcccttttct	ccaacacaca	catttgtctc	gtggggtggg	-401
10	-400	ggttaaacat	ggggggaggga	ggaaagggat	aggatagaga	atgggagtgtg	-351
	-350	gtgctgtagg	ggttctcaagg	actggctatc	ctgaactcct	tctccgcgtt	-301
	-300	caaggtgtagg	accatggcct	cgccggcagag	ggcaccacag	tgacctctaa	-251
	-250	agagaggagca	agtgtgggtg	tatctctggc	tgacaactctg	tgcaacaacc	-201
	-200	tcacacacat	ggtgacggtg	ggaaagggaaa	gatgacaagc	caggggggcat	-151
15	-150	gacccacaga	tgtgtgggag	gagcttctaa	attatccatt	agcacaagcc	-101
	-100	cgteagtggc	cccattgcata	aatgtacaca	gaacacaggtg	gggggcaacg	-51
	-50	tgggagagaaa	ggggccaggg	tataaaaaagg	gccacaaga	gaccagctca	-1
	+1	aggtacccaa	ggcccaactc	cccgaaccac	tcaagggtcct	gtggacagct	+50
20	+51	caactagcgg	caATGCTTAC	AGgtaagcgc	ccctaaaato	cctttggggca	+100
	+101	caatgtgtctc	tgaggggaga	ggcagcgacc	tgtagatggg	acggggggcac	+150
	+151	taacccctcag	gtttggggct	tctgaatgtg	agtatcgcca	tgtaacccca	+200
	+201	gtattttggcc	aattctcagaa	agctcctggt	ccctggaggg	atggagagag	+250
	+251	aaaaaaccaa	agctcctgga	gcaggggagag	tgtctggctc	tgtctctcgc	+300
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	+351	TGCTGGCTTT	TGCTGCTGCTC	TGCTGCTGCTC	GGCTTCAAGA	GGGCACTGCC	+400
	+401	TTCCCAACCA	TTCCCTTATC	CAGGCTTTTT	GACAACGCTA	TGCTCCGCGC	+450
	+451	CCATCGTCTG	CACCAGCTGG	CCTTTGACAC	TACCAGAGAG	TTTgtaagct	+500
	+501	ctttggggaaat	gggtgcgcac	caggggtggc	aggaaagggg	gactttcccc	+550
	+551	cgctggggaaa	taagaggagg	agactaaaga	gctccagggtt	tctcccgaa	+600
30	+601	cgaaaaatgca	ggcagatgag	cacacgctga	gtgagggttcc	cagaaaaagt	+650
	+651	acagtgtggag	ctggtctcca	gcgtagacct	tgggtggcgg	tcttctctct	+700
	+701	agGAAGAGC	CTATATCCCA	AAGGAACAGA	AGTATTTCAT	CCTGCAGAAC	+750
	+751	CCCCAGACT	CCCTCTGTTT	CTCAGAGTCT	ATTCCGACAC	CCTCCAACAG	+800
	+801	GGAGGAACA	CAACAGAAAT	CCgtgagtg	atgcctcttc	cccaggcggg	+850
35	+851	gatcgggggag	acctgtagtc	agagcccccg	ggcagcacag	ccaatgcccg	+900
	+901	tcctctcccc	cgagAACCTA	GAGCTGCTCC	GCATCTCCCT	GCTGCTCATC	+950
	+951	CAGTCGTGGC	TGGAGCCCGT	GCAGTTCCTC	AGGAGTGTCT	TGCGCAACAG	+1000
	+1001	CCTGTGTIAC	GGCGCCTCTG	ACAGCAACGT	CTATGACCTC	CTAAAGGACC	+1050
	+1051	TAGAGGAAGG	CATCCAAACG	CTGATGGGGG	tgagggtggc	gccagggggtc	+1100
40	+1101	ccccattctg	gagccccact	gactttgaga	gctgtgttag	agaaacactg	+1150
	+1151	ctgcctcttt	tttagcagtc	agggcctgac	ccaagagaac	tcacctattt	+1200
	+1201	cttcatttcc	cctcgtgaat	cctccaggcc	tttctctaca	ccctgaaggg	+1250
	+1251	gagggaggaa	aatgaatgaa	tgagaaaggg	aggggaacagt	acccaagcgc	+1300
	+1301	ttggcctctc	cttctctctc	ttcactttgc	agAGGCTGGA	AGATGGCAGC	+1350
45	+1351	CCCCGAGCTG	GGCAGATCTT	CAAGCAGACC	TACAGCAAGT	TCGACACAAA	+1400
	+1401	CTCACACAC	GATGACGCAC	TACTCAAGAA	CTACGGGGCTG	CTCTACTGCT	+1450
	+1451	TCAGGAAGGA	CATGGACAAG	GTGAGACATC	TCCCTGCGCAT	CGTGCACTGC	+1500
	+1501	CGCTCTGTGG	AGGGCAGCTG	TGGCTTCTAG	gtcccccgggt	ggcatccctg	+1550
	+1551	tgaccctctc	ccagtcctct	ctcctggcctc	ggaaagtggc	actccaagtc	+1600
50	+1601	ccacacagcct	tgtcctaat	aaattaagtt	gcatactttt	gtctgactag	+1650
	+1651	gtgtctctct	ataataattt	gggggtggaag	gggggtggtat	ggagacaagg	+1700
	+1701	gcaagtgtgg	aagacaacct	gtaggggcctg	cggggtctat	tcgggaaacca	+1750
	+1751	agctggagtg	cagtgggaca	attctggctc	actgcaactc	cgccctcctg	+1800
	+1801	ggttccaagcg	attctctcgc	ctcagcctcc	cgagttgtgt	ggattccaag	+1850
55	+1851	catcgcatgac	caggctcagc	taatttttgt	tttttgttgt	gagacgggggt	+1900
	+1901	ttccaacatc	tggccaggct	ggtctccaac	tcctaatctc	aggtgatctc	+1950
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	+2151	tgttggaattc	ctggggcctag	ggctgtgcca	gctgcctcgt	cccgctcact	+2200
	+2201	tctgtgctct	ctctctccct	catatcttag	ctgttttctc	catgagaagt	+2250
	+2251	ttccaaattc	gaaattctta	tttaaccatt	atatatttac	tgtgttgcta	+2300

**Figure 5 (continued)**

5	+2301	ttatctctgc	ccccagtaga	ttgttagctc	cagaagagaa	aggatcatgt	+2350
	+2351	cttttgctta	tctagatatg	cccatctgcc	tggtacaatc	tctggcacat	+2400
	+2401	gttacaggca	acaactactt	gtggaattgg	tgaatgcatg	aatagaagaa	+2450
	+2451	tgagtgaatg	aatgaataga	caaaaggcag	aatccagcc	tcaaagaact	+2500
	+2501	tacagtctgg	taaggaggaat	aaaatgtctg	caaatagcca	caggacaggt	+2550
10	+2551	caaaagggaag	aggggctatt	tccagctgag	ggcaccocat	caggaaagga	+2600
	+2601	ccccagactt	cctacaacta	ctagacacat	ctcgatgctt	ttcacttctc	+2650
	+2651	tatcaatgga	tctgtctcct	ggagaataat	ccccaaagtg	aaattactta	+2700
	+2701	gcacgtccag	ttaggtagat	ccttgtgtac	ttcttggttg	ttcagagatc	+2750
	+2751	atcaaccagt	gcaaacacac	cccccatcaa	tacacagcag	tgccctgccc	+2800
15	+2801	tctccccccg	aggtcttccg	agggccttcc	tccgtgctg	aacccccctg	+2850
	+2851	acatatcata	tggcaaaactg	aagtgtccaa	cgagatatag	gaagtgaaac	+2900
	+2901	acgatgtaca	ctgaaacgtg	caatacaaat	atgcagcatg	aagtgcctcg	+2950
	+2951	gttcactaac	ccgagctacg	ctgggtgctt	cttttctacc	actttcetta	+3000

20

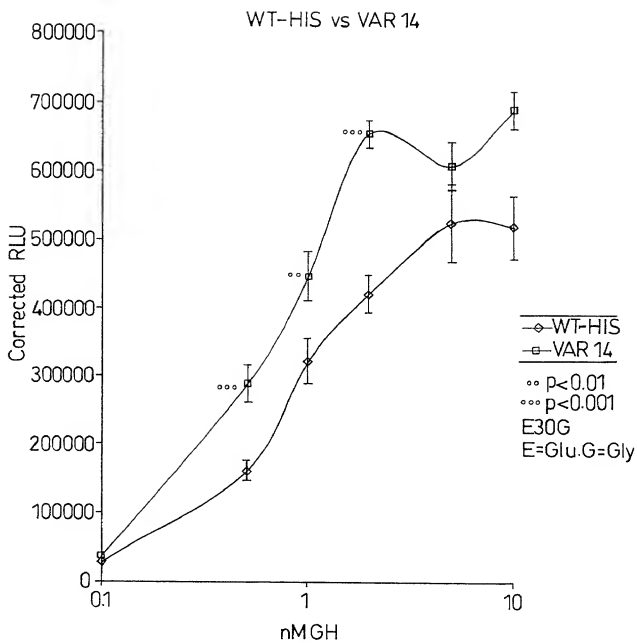


**Figure 6**

Growth hormone 1		
Gene symbol : <i>GH1</i>		
Location : 17q		
	1 2	
-26	ATG GCT ACA G↓GC TCC CGG ACG TCC CTG CTC CTG GCT TTT GGC CTG	-12
	Met Ala Thr G Iy Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu	
10	-11 CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC TTC CCA ACC ATT	4
	Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile	
15	5 CCC TTA TCC AGG CTT TTT GAC AAC GCT AGT CTC CGC GCC CAT CGT	19
	Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg	
	2 3	
20	CTG CAC CAG CTG GCC TTT GAC ACC TAC CAG GAG TTT ↓ GAA GAA GCC	34
	Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala	
20	35 TAT ATC CCA AAG GAA CAG AAG TAT TCA TTC CTG CAG AAC CCC CAG	49
	Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln	
50	ACC TCC CTC TGT TTC TCA GAG TCT ATT CCG ACA CCC TCC AAC AGG	64
	Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg	
25	3 4	
65	GAG GAA ACA CAA CAG AAA TCC ↓ AAC CTA GAG CTG CTC CGC ATC TCC	79
	Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser	
80	CTG CTG CTC ATC CAG TCG TGG CTG GAG CCC GTG CAG TTC CTC AGG	94
30	Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg	
95	AGT GTC TTC GCC AAC AGC CTG GTG TAC GGC GCC TCT GAC AGC AAC	109
	Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn	
35	110 GTC TAT GAC CTC CTA AAG GAC CTA GAG GAA GGC ATC CAA ACG CTG	124
	Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu	
	4 5	
125	ATG GGG ↓ AGG CTG GAA GAT GGC AGC CCC CGG ACT GGG CAG ATC TTC	139
	Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe	
40	140 AAG CAG ACC TAC AGC AAG TTC GAC ACA AAC TCA CAC AAC GAT GAC	154
	Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp	
155	GCA CTA CTC AAG AAC TAC GGG CTG CTC TAC TGC TTC AGG AAG GAC	169
45	Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp	
170	ATG GAC AAG GTC GAG ACA TTC CTG CGC ATC GTG CAG TGC CGCTCT	184
	Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser	
50	185 GTG GAG GGC AGC TGT GGC TTC TAG	
	Val Glu Gly Ser Cys Gly Phe *	

**Figure 7**

GH variant <i>Glu-Gly30</i>	
Location: 17q	
5	<div>1 2</div> <div>-26 ATG GCT ACA G<sup>1</sup>GC TCC CGG ACG TCC CTG CTC CTG GCT TTT GGC CTG -12</div> <div>Met Ala Thr G ly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu</div>
10	<div>-11 CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC TTC CCA ACC ATT 4</div> <div>Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile</div>
15	<div>5 CCC TTA TCC AGG CTT TTT GAC AAC GCT AGT CTC CGC GCC CAT CGT 19</div> <div>Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg</div> <div>2 3</div> <div>20 CTG CAC CAG CTG GCC TTT GAC ACC TAC CAG GAG TTT ↓ <i>GGG</i> GAA GCC 34</div> <div>Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe <i>Gly</i> Glu Ala</div>
20	<div>35 TAT ATC CCA AAG GAA CAG AAG TAT TCA TTC CTG CAG AAC CCC CAG 49</div> <div>Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln</div>
25	<div>50 ACC TCC CTC TGT TTC TCA GAG TCT ATT CCG ACA CCC TCC AAC AGG 64</div> <div>Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg</div> <div>3 4</div> <div>65 GAG GAA ACA CAA CAG AAA TCC ↓ AAC CTA GAG CTG CTC CGC ATC TCC 79</div> <div>Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser</div>
30	<div>80 CTG CTG CTC ATC CAG TCG TGG CTG GAG CCC GTG CAG TTC CTC AGG 94</div> <div>Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg</div>
35	<div>95 AGT GTC TTC GCC AAC AGC CTG GTG TAC GGC GCC TCT GAC AGC AAC 109</div> <div>Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn</div>
40	<div>110 GTC TAT GAC CTC CTA AAG GAC CTA GAG GAA GGC ATC CAA ACG CTG 124</div> <div>Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu</div> <div>4 5</div> <div>125 ATG GGG ↓ AGG CTG GAA GAT GGC AGC CCC CGG ACT GGG CAG ATC TTC 139</div> <div>Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe</div>
45	<div>140 AAG CAG ACC TAC AGC AAG TTC GAC ACA AAC TCA CAC AAC GAT GAC 154</div> <div>Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp</div>
50	<div>155 GCA CTA CTC AAG AAC TAC GGG CTG CTC TAC TGC TTC AGG AAG GAC 169</div> <div>Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp</div>
	<div>170 ATG CAG AAG GTC GAG ACA TTC CTG CGC ATC GTG CAG TGC CGC TCT 184</div> <div>Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser</div>
	<div>185 GTG GAG GGC AGC TGT GGC TTC TAG</div> <div>Val Glu Gly Ser Cys Gly Phe *</div>



**Fig. 8**